

#### SEQUENCE LISTING

### (1) GENERAL INFORMATION:

(i) APPLICANT: LITTMAN, DAN R.

DENG, HONGKUI

ELLMEIER, WILFRIED

ELLMEIER, WILFRIED LANDAU, NATHANIEL R.

LIU, RONG

- (ii) TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH MACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: David A. Jackson, Esq.
  - (B) STREET: 411 Hackensack Ave, Continental Plaza, 4th Floor
  - (C) CITY: Hackensack
  - (D) STATE: New Jersey
  - (E) COUNTRY: USA
  - (F) ZIP: 07601
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: 09/734,221
  - (B) FILING DATE:2000/12/11
  - (C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/666,020
  - (B) FILING DATE: 19-JUN-1996
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/227,319
  - (B) FILING DATE: 13-APR-1994
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Jackson Esq., David A.
  - (B) REGISTRATION NUMBER: 26,742
  - (C) REFERENCE/DOCKET NUMBER: 1049-1-004 N2
  - (ix) TELECOMMUNICATION INFORMATION:
    - (A) TELEPHONE: 201-487-5800
    - (B) TELEFAX: 201-343-1684
- (2) INFORMATION FOR SEQ ID NO:1:

	<ul><li>(A) LENGTH: 29 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iii)	HYPOTHETICAL: NO	
(vi)	ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1:	
CTCGGATC	CG GTGGAACAAG ATGGATTAT	29
(2) INFO	RMATION FOR SEQ ID NO:2:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 28 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iii)	HYPOTHETICAL: NO	
(vi)	ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:2:	
CTCGTCGA	CA TGTGCACAC TCTGACTG	28
(2) INFO	RMATION FOR SEQ ID NO:3:	
	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 66 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(iii)	HYPOTHETICAL: NO	
(vi)	ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:3:	
\TGGATTAT	CC AAGTGTCAAG TCCAATCTAT GACATCAATT ATTATACATC GGAGCCCTGC	60

(i) SEQUENCE CHARACTERISTICS:

CAAAAA 66

CAA	AAA		6
(2)	INFO	RMATION FOR SEQ ID NO:4:	
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 22 amino acids  (B) TYPE: amino acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: peptide	
	(iii)	HYPOTHETICAL: NO	
	(v)	FRAGMENT TYPE: internal	
	(vi)	ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:4:	
	Met 1	Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr 5 10 15	
	Ser	Glu Pro Cys Gln Lys 20	
(2)	INFO	RMATION FOR SEQ ID NO:5:	
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 84 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	
	(iii)	HYPOTHETICAL: NO	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:5:	
		TC AAGTGTCAAG TCCAATCTAT GACATCAATT ATCCATACGA TGTTCCAGAT GG AGCCCTGCCA AAAA	6 · 8 ·
(2)	INFO	RMATION FOR SEQ ID NO:6:	
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 28 amino acids  (B) TYPE: amino acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: peptide	

(iii) HYPOTHETICAL: NO
 (v) FRAGMENT TYPE: internal

	Met 1	Asp	Tyr	Gln	Val 5	Ser	Ser	Pro	Ile	Tyr 10	Asp	Ile	Asn	Tyr	Pro 15	Tyr	
	Asp	Val	Pro	Asp 20	Tyr	Ala	Ser	Glu	Pro 25	Cys	Gln	Lys					
(2)	INFOF	ITAMS	ON I	FOR S	SEQ :	ID NO	0:7:										
	(i)	(A) (B) (C)	LEN TYI STI	NGTH: PE: r RANDE	: 51 nucle EDNES	TERIS base eic a SS: s linea	e pai acid singl	rs									
	(ii)					other N: /c					.eoti	.des"	1				
i )	Lii)	нүрс	THET	CICAL	.: NC												
ı	(vi)					: Iomo	sapi	.ens									
ı	(xi)	SEQU	ENCE	DES	CRIE	MOIT	: SE	Q II	NO:	7:							
ATCA	TATTA	C CA	TACC	SATGT	TCC	CAGAT	TAT	GCTI	'CGGA	.GC C	CTGC	CAAA	A A				51
(2) ]	NFOR	MATI	ON F	OR S	EQ I	D NC	8:										
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 63 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>																
(	(ii)					ther : /d				-	eoti	des"					
(i	ii)	НҮРО	THET	'ICAL	: NC	)											
(	vi)					omo	sapi	ens									
(	xi)	SEQU	ENCE	DES	CRIP	TION	: SE	Q ID	NO:	8:							
GCAGG GAT	ATCC	A CC.	ATGG	ATTA	TCA	AGTG	TCA	AGTC	CAAT	CT A	TGAC	ATCA	A TT	ATCC	ATAC		60 63
(2) I	NFOR	MATI	ON F	or s	EQ I	D NO	:9:										
	(i)	(A) (B) (C)	LEN TYP STR	GTH: E: n ANDE	24 ucle DNES	ERIS base ic a S: d inea	pai cid oubl	rs									

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

(ii)	MOLECULE TYPE: cDNA	
(iii)	HYPOTHETICAL: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:9:	
CCATACGA	TG TTCCAGATTA TGCT	24
(2) INFO	RMATION FOR SEQ ID NO:10:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 8 amino acids  (B) TYPE: amino acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: peptide	
(iii)	HYPOTHETICAL: NO	
(v)	FRAGMENT TYPE: internal	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:10:	
Pro 1	Tyr Asp Val Pro Asp Tyr Ala 5	
(2) INFO	RMATION FOR SEQ ID NO:11:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 30 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(iii)	HYPOTHETICAL: NO	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:11:	
TATCCATA	CG ATGTTCCAGA TTATGCTTCG	30
(2) INFO	RMATION FOR SEQ ID NO:12:	
	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 10 amino acids  (B) TYPE: amino acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: peptide	
(iii)	HYPOTHETICAL: NO	
(v)	FRAGMENT TYPE: internal	

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser 1 5 10

## (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3383 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGAAGAGCTG	AGACATCCGT	TCCCCTACAA	GAAACTCTCC	CCGGGTGGAA	CAAGATGGAT	60
				CATCGGAGCC		120
ATCAATGTGA	AGCAAATCGC	AGCCCGCCTC	CTGCCTCCGC	TCTACTCACT	GGTGTTCATC	180
${\tt TTTGGTTTTG}$	TGGGCAACAT	GCTGGTCATC	CTCATCCTGA	TAAACTGCAA	AAGGCTGAAG	240
AGCATGACTG	ACATCTACCT	GCTCAACCTG	GCCATCTCTG	ACCTGTTTTT	CCTTCTTACT	300
GTCCCCTTCT	GGGCTCACTA	TGCTGCCGCC	CAGTGGGACT	TTGGAAATAC	AATGTGTCAA	360
CTCTTGACAG	GGCTCTATTT	TATAGGCTTC	TTCTCTGGAA	TCTTCTTCAT	CATCCTCCTG	420
ACAATCGATA	GGTACCTGGC	TGTCGTCCAT	$\tt GCTGTGTTTG$	CTTTAAAAGC	CAGGACGGTC	480
ACCTTTGGGG	TGGTGACAAG	TGTGATCACT	TGGGTGGTGG	CTGTGTTTGC	GTCTCTCCCA	540
GGAATCATCT	TTACCAGATC	TCAAAAAGAA	GGTCTTCATT	ACACCTGCAG	CTCTCATTTT	600
CCATACAGTC	AGTATCAATT	CTGGAAGAAT	TTCCAGACAT	TAAAGATAGT	CATCTTGGGG	660
CTGGTCCTGC	CGCTGCTTGT	CATGGTCATC	TGCTACTCGG	GAATCCTAAA	AACTCTGCTT	720
CGGTGTCGAA	ATGAGAAGAA	GAGGCACAGG	GCTGTGAGGC	TTATCTTCAC	CATCATGATT	780
GTTTATTTTC	TCTTCTGGGC	TCCCTACAAC	ATTGTCCTTC	TCCTGAACAC	CTTCCAGGAA	840
TTCTTTGGCC	TGAATAATTG	CAGTAGCTCT	AACAGGTTGG	ACCAAGCTAT	GCAGGTGACA	900
GAGACTCTTG	GGATGACGCA	CTGCTGCATC	AACCCCATCA	TCTATGCCTT	TGTCGGGGAG	960
AAGTTCAGAA	ACTACCTCTT	AGTCTTCTTC	CAAAAGCACA	TTGCCAAACG	CTTCTGCAAA	1020
TGCTGTTCTA	TTTTCCAGCA	AGAGGCTCCC	GAGCGAGCAA	GCTCAGTTTA	CACCCGATCC	1080
ACTGGGGAGC	AGGAAATATC	TGTGGGCTTG	TGACACGGAC	TCAAGTGGGC	TGGTGACCCA	1140
GTCAGAGTTG	TGCACATGGC	TTAGTTTTCA	TACACAGCCT	GGGCTGGGGG	TGGGGTGGGA	1200
GAGGTCTTTT	TTAAAAGGAA	GTTACTGTTA	TAGAGGGTCT	AAGATTCATC	CATTTATTTG	1260
GCATCTGTTT	AAAGTAGATT	AGATCTTTTA	AGCCCATCAA	TTATAGAAAG	CCAAATCAAA	1320
ATATGTTGAT	GAAAAATAGC	AACCTTTTTA	TCTCCCCTTC	ACATGCATCA	AGTTATTGAC	1380
AAACTCTCCC	TTCACTCCGA	AAGTTCCTTA	TGTATATTTA	AAAGAAAGCC	TCAGAGAATT	1440
GCTGATTCTT	GAGTTTAGTG	ATCTGAACAG	AAATACCAAA	ATTATTTCAG	AAATGTACAA	1500
CTTTTTACCT	AGTACAAGGC	AACATATAGG	TTGTAAATGT	GTTTAAAACA	GGTCTTTGTC	1560
TTGCTATGGG	GAGAAAAGAC	ATGAATATGA	TTAGTAAAGA	AATGACACTT	TTCATGTGTG	1620
ATTTCCCCTC	CAAGGTATGG	TTAATAAGTT	TCACTGACTT	AGAACCAGGC	GAGAGACTTG	1680
${\tt TGGCCTGGGA}$	GAGCTGGGGA	AGCTTCTTAA	ATGAGAAGGA	ATTTGAGTTG	GATCATCTAT	1740
TGCTGGCAAA	GACAGAAGCC	TCACTGCAAG	CACTGCATGG	GCAAGCTTGG	CTGTAGAAGG	1800
AGACAGAGCT	GGTTGGGAAG	ACATGGGGAG	GAAGGACAAG	GCTAGATCAT	GAAGAACCTT	1860
GACGGCATTG	${\tt CTCCGTCTAA}$	GTCATGAGCT	GAGCAGGGAG	ATCCTGGTTG	GTGTTGCAGA	1920
AGGTTTACTC	TGTGGCCAAA	GGAGGGTCAG	${\tt GAAGGATGAG}$	CATTTAGGGC	AAGGAGACCA	1980
CCAACAGCCC	TCAGGTCAGG	${\tt GTGAGGATGG}$	${\tt CCTCTGCTAA}$	GCTCAAGGCG	TGAGGATGGG	2040

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AAGGAGGGAG	GTATTCGTAA	GGATGGGAAG	GAGGGAGGTA	TTCGTGCAGC	ATATGAGGAT	2100
GCAGAGTCAG	CAGAACTGGG	GTGGATTTGG	TTTGGAAGTG	AGGGTCAGAG	AGGAGTCAGA	2160
GAGAATCCCT	AGTCTTCAAG	CAGATTGGAG	AAACCCTTGA	AAAGACATCA	AGCACAGAAG	2220
GAGGAGGAGG	AGGTTTAGGT	CAAGAAGAAG	ATGGATTGGT	GTAAAAGGAT	GGGTCTGGTT	2280
TGCAGAGCTT	GAACACAGTC	TCACCCAGAC	TCCAGGCTGT	CTTTCACTGA	ATGCTTCTGA	2340
CTTCATAGAT	TTCCTTCCCA	TCCCAGCTGA	AATACTGAGG	GGTCTCCAGG	AGGAGACTAG	2400
ATTTATGAAT	ACACGAGGTA	TGAGGTCTAG	GAACATACTT	CAGCTCACAC	ATGAGATCTA	2460
GGTGAGGATT	GATTACCTAG	TAGTCATTTC	ATGGGTTGTT	GGGAGGATTC	TATGAGGCAA	2520
CCACAGGCAG	CATTTAGCAC	ATACTACACA	TTCAATAAGC	ATCAAACTCT	TAGTTACTCA	2580
TTCAGGGATA	GCACTGAGCA	AAGCATTGAG	CAAAGGGGTC	CCATATAGGT	GAGGGAAGCC	2640
TGAAAAACTA	AGATGCTGCC	TGCCCAGTGC	ACACAAGTGT	AGGTATCATT	TTCTGCATTT	2700
AACCGTCAAT	AGGCAAAGGG	GGGAAGGGAC	ATATTCATTT	GGAAATAAGC	TGCCTTGAGC	2760
CTTAAAACCC	ACAAAAGTAC	AATTTACCAG	CCTCCGTATT	TCAGACTGAA	TGGGGGTGGG	2820
GGGGGCGCCT	TAGGTACTTA	TTCCAGATGC	CTTCTCCAGA	CAAACCAGAA	GCAACAGAAA	2880
AAATCGTCTC	TCCCTCCCTT	TGAAATGAAT	ATACCCCTTA	GTGTTTGGGT	ATATTCATTT	2940
CAAAGGGAGA	GAGAGAGGTT	TTTTTCTGTT	CTTTCTCATA	TGATTGTGCA	CATACTTGAG	3000
ACTGTTTTGA	ATTTGGGGGA	TGGCTAAAAC	CATCATAGTA	CAGGTAAGGT	GAGGGAATAG	3060
TAAGTGGTGA	GAACTACTCA	GGGAATGAAG	GTGTCAGAAT	AATAAGAGGT	GCTACTGACT	3120
TTCTCAGCCT	CTGAATATGA	ACGGTGAGCA	TTGTGGCTGT	CAGCAGGAAG	CAACGAAGGG	3180
AAATGTCTTT	CCTTTTGCTC	TTAAGTTGTG	GAGAGTGCAA	CAGTAGCATA	GGACCCTACC	3240
CTCTGGGCCA	AGTCAAAGAC	ATTCTGACAT	CTTAGTATTT	GCATATTCTT	ATGTATGTGA	3300
AAGTTACAAA	TTGCTTGAAA	GAAAATATGC	ATCTAATAAA	AAACACCTTC	TAAAATAAAA	3360
AAAAAAAAA	AAAAAAAAA	AAA				3383
	GCAGAGTCAG GAGAATCCCT GAGGAGGAGG TGCAGAGCTT CTTCATAGAT ATTTATGAAT GGTGAGGATA TCAGGGATA TGAAAAACTA AACCGTCAAT CTTAAAACCC GGGGGCGCCT AAATCGTCTC CAAAGGGAGA ACTGTTTTGA TAAGTGGTGA TTCTCAGCCT AAATGTCTTT CTCTGGGCCA AAGTTACAAA	GCAGAGTCAG CAGAACTGGG GAGAATCCCT AGTCTTCAAG GAGGAGGAGG AGGTTTAGGT TGCAGAGCTT GAACACAGTC CTTCATAGAT TTCCTTCCCA ATTTATGAAT ACACGAGGTA GGTGAGGATT GATTACCTAG CCACAGGCAG CATTTAGCAC TTCAGGGATA GCACTGAGCA TGAAAAACTA AGATGCTGCC AACCGTCAAT AGGCAAAGGG CTTAAAACCC ACAAAAGTAC GGGGGCGCCT TAGGTACTTA AAATCGTCTC TCCCTCCCTT CAAAGGGAGA GAGAGAGGTT ACTGTTTTGA ATTTGGGGGA TAAGTGGTGA GAACTACTCA TTCTCAGCCT CTGAATATGA AAATGTCTTT CCTTTTGCTC CTCTGGGCCA AGTCAAAGAC AAGTTACAAA	GCAGAGTCAG CAGAACTGGG GTGGATTTGG GAGAATCCCT AGTCTTCAAG CAGATTGGAG GAGGAGGGG AGGTTTAGGT CAAGAAGAAG TGCAGAGCTT GAACACAGTC TCACCCAGAC CTTCATAGAT TTCCTTCCCA TCCCAGCTGA ATTTATGAAT ACACGAGGTA TGAGGTCTAG GGTGAGGATT GATTACCTAG TAGTCATTTC CCACAGGCAG CATTTAGCAC ATACTACACA TTCAGGGATA GCACTGAGCA AAGCATTGAG TGAAAAACTA AGATGCTGC TGCCCAGTGC AACCGTCAAT AGGCAAAGGG GGGAAGGGAC CTTAAAACCC ACAAAAGTAC AATTTACCAG GGGGGCGCCT TAGGTACTTA TTCCAGATGC AAATCGTCTC TCCCTCCCTT TGAAATGAAT CAAAGGGAGA GAGAGAGGTT TTTTTCTGTT ACTGTTTTGA ATTTGGGGGA TGGCTAAAAC TAAGTGGTGA GAACTACTCA GGGAATGAAG TTCTCAGCCT CTGAATATGA ACGGTGAGCA AAATGTCTTT CCTTTTGCTC TTAAGTTGTG CTCTGGGCCA AGTCAAAGAC ATTCTGACAT	GCAGAGTCAG CAGAACTGGG GTGGATTTGG TTTGGAAGTG GAGAATCCCT AGTCTTCAAG CAGATTGGAG AAACCCTTGA GAGGAGGAG AGGTTTAGGT CAAGAAGAAG ATGGATTGGT TGCAGAGCTT GAACACAGTC TCACCCAGAC TCCAGGCTGT CTTCATAGAT TTCCTTCCCA TCCCAGCTGA AATACTGAGG ATTTATGAAT ACACGAGGTA TGAGGTCTAG GAACATACTT GGTGAGGATT GATTACCTAG TAGTCATTC ATGGGTTGTT CCACAGGCAG CATTTAGCAC ATACTACACA TTCAATAAGC TTCAGGGATA GCACTGAGCA AAGCATTGAG CAAAGGGGTC TGAAAAACTA AGGTGACAC AGCCATTGAG CAAAGGGGTC AACCGTCAAT AGGCAAAGGG GGGAAGGAC ATATTCATTT CTTAAAACCC ACAAAAGTAC AATTTACCAG CCTCCGTATT GGGGGCGCCT TAGGTACTTA TTCCAGATGC CTTCTCCAGA AAATCGTCTC TCCCTCCTT TGAAATGAAT ATACCCCTTA ACTGTTTTGA ATTTGGGGGA TGGCTAAAAC CATCATAGTA TAAGTGGTGA GAACTACTCA GGGAATGAAG GTGTCAGAAT TTCTCAGCCT CTGAATATGA ACGGTGAGCA TTGTGGCTGT TAAGTGGTCA AGCCATAGTA ACGGTGAGCA TTGTGGCTGT TAAGTGGTCA AGCCATAGTA ACGGTGAGCA TTGTGGCTGT AAATGTCTTT CCTTTTGCTC TTAAGTTGTG GAGAGTGCAA CTCTGGGCCA AGTCAAAGAC ATTCTGACAT CTTAGTATTT AAGTTGCAAA TTGCTTGAAA CCTTAATAAA	GCAGAGTCAG CAGAACTGGG GTGGATTTGG TTTGGAAGTG AGGGTCAGAG GAGAATCCCT AGTCTTCAAG CAGATTGGAG AAACCCTTGA AAAGACATCA GAGGAGGAGG AGGTTTAGGT CAAGAAGAAG ATGGATTGGT GTAAAAGGAT TCACCAGAGCTT GAACACAGTC TCACCCAGAC TCCAGGCTGT CTTTCACTGA ATTGATAGAT ACACGAGGTA TGAGGTCTAG GAACATACT CAGCTCACAC GGTGAGGATT GATTACCTAG TAGTCATTC ATGGGTTGTT GGGAGGATTC CACCAGAGCTT GATTACCACA TTCAATAAGC ATCAAACTCT CAGCTCACAC GGTGAGGATT GATTACCTAG TAGTCATTTC ATGGGTTGTT GGGAGGATTC CCACAGGCAG CATTTAGCAC ATACTACACA TTCAATAAGC ATCAAACTCT TCCAGGGATA GCACTGAGCA AAGCATTGAG CAAAGGGGTC CCATATAGGT TGAAAAAACTA AGATGCTGCC TGCCCAGTGC ACACAAGTGT AGGTATCATT AACCCGTCAAT AGGCAAAGGG GGGAAGGGAC ATATTCATTT GGAAATAAGC CTTAAAACCC ACAAAAGTAC AATTTACCAG CCTCCGTATT TCAGACTGAA AAATCGTCTC TCCCTCCTT TGAAATGAAT ATACCCCTTA GTGTTTGGGT CAAAGGGAG GAGAGGAGT TTTTTCTGTT CTTTCCAGA CAAACCAGAA ACTGTTTTGA ATTTGGGGGA TGGCTAAAAC CATCATAGTA CAGGTAAGGT TAGTGTTTGAAAACCA ATTTTCATTT GAAATGAAT ATACCCCTTA TGATTTGGGT TAAAGTGGTA ATTTGGGGGA TTTTTCTGTT CTTTCCATA TGATTTGGGT TAAAGTGGTA ATTTGGGGA TGGCTAAAAC CATCATAGTA CAGGTAAAGGT TAAGTGGTGA GAACTACTCA GGGAATGAAA CTTTCTCATA TGATTTGGGT CAGCAGAAGTT TTTTCTGTT CTTTCCATA TGATTTGGGT CAGCAGAAGTT TTTTCTGTT CTTTCCATA AATAAGAGGT TTCTCAGCCT CTGAATATGA ACGGTGAGA TTGTGGCTGT CAGCAGGAAG AAATGTCTT CTGAAATAGA ACGGTGAGA TTGTGGCTGT CAGCAGGAAG AAATGTCTT CTTTGCTC TTAAGTTGTG GAGAGTGCAA CAGTAAGAAC CAGCAGGAAG AAATGTCTTT CTTTTGCTC TTAAGTTTTT GCATATTCTT AAGTTCTT AAGTTGTG GAGAGTGCAA CAGTAGCATA AATAACACCTTCT AAGTTACAAA TTGCTTGAAAAAAAAAA	GCAGAGTCAG CAGAACTGGG GTGGATTTGG TTTGGAAGTG AGGGTCAGAG AGGAGTCAGAG GAGAATCCCT AGTCTTCAAG CAGATTGAGG AAACCCTTGA AAAGACATCA AGCACAGAAG GAGGAGGAGG AGGTTTAGGT CAAGAAGAAG ATGGATTGGT GTAAAAGGAT GGGTCTGGTT TGCAGAGCTT GAACACAGTC TCCACGACC TCCAGGCTGT CTTTCACTGA ATGCTTCTGA ATTTATGAAT ACACGAGGTA TGAGGTCTAG GAACACAGTC TCCAGGCTGT CTTTCACTGA AGGAGACTAG AGGAGACTAG AGGAGACTAG GGGTCACAG AGGAGACTAG GGGTGAGGATT GATTACCTAG TAGTCATTC ATGGGTTGTT GGGAGGATTC TATGAGGCAA ATACTACACA TTCAATAAGC ATCAAACTCT TAGTTACTCA ACACGAGGAA AGCACTAGCA ACACAAGTGT AGGAACACACA TCCAAGGCAG CATTTAGCAC ATACTACACA TTCAATAAGC ATCAAACTCT TAGTTACTCA ACCGTCAAT AGGCAAAAGGG GGGAAGGCC ACACAAGTGT AGGTATCATT TCTTGCATTT AACCGTCAAT AGGCAAAGGG GGGAAGGGAC ATATTCATTT GGAAAAACTA AGGCAAAAGGG GGGAAGGGAC ATATTCATTT GGAAATAAGC TCCCTTGAGC ACACAAGTGT AGGTATCATT TCTTGCATTT AACCGTCAAT AGGCAAAAGTAC AATTTACCAG CCTCCGTATT TCAGACTGAA TGGGGGTGGG GGGGGGGGCCCT TAGGTACTTA TTCCAGATGC CTTCTCCAGA CAAACCAGAA GCAACAGAAA AAATCGTCTC TCCCTCCTTT TGAAATGAAT ATACCCCTTAA TGATTGTGCA CATACTTGAG ACTGTTTTGA ATTTCATTT TCAAAATGAAT ATACCCCTTA TGATTGTGCA CATACTTGAG ACTGTTTTGA ATTTCATTT CTTTCTCATA TGATTGTGCA CATACTTGAG ACTGTTTTTGA ATTTCATTT GAGAGTGAA AATTAGAGG GAGAATAAGC TCTCTCAGAC AAACCAGAA AATTTCATTT CTTTCTTTTTAGA ATTTCATTT AAACTCAG CATACTTCAGC CTTCTCAGAC AAACCAGAA AATTTCATTT CTTTCTTTTTTTTTT

### (2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 352 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
1 5 10 15

Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu 20 25 30

Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn 35 40 45

Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met 50 55 60

Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu 65 70 75 80

Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe

85

Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe 105 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu 120 Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe 135 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser 150 155 160 Leu Pro Gly Ile -Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn 185 Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu 195 200 Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys 215 Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile 230 235 240 Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser 265 Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr 275 280 His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe 295 Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe 305 315 Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser Ser Val Tyr Thr Arg Ser Thr Gly Glu Glu Glu Ile Ser Val Gly Leu